

FIGURE 1

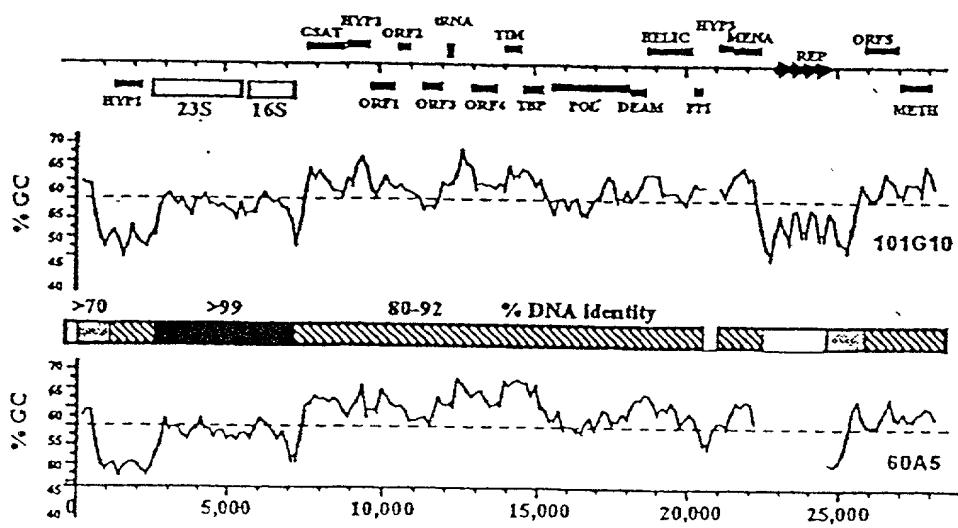


Figure 2

| Gene | Strain | TATA Box | Coding Start | TATA to Start (b) |
|-----------------------------|--------|---|--------------|-------------------|
| 81 Hypoth 03 | A | AAGCTAGACT TTTAAT TGGG ATCCGGCGGG GCGGGCGCATG | ----- | 25 |
| 82 | B | AAGCTAACT TTTAAT TGGG ATCCGGCGAG CCGGGCGCGT | ----- | |
| 83 Hypoth 02 | A | GGAAACTTTG ATTATA CGGG CGTGCTGCC CGGGGCCAT G----- | | 26 |
| 84 | B | GGAAACTTTG ATTATA CGGG CGTACATTCC CGGGGCCAT G----- | | |
| 85 ORF 02 | A | AAGGCAAGGT AATAAT AGCC TGCGCTCTGT AACGGCCGTA TG----- | | 27 |
| 86 | B | ACGGCAAGGT AATAAT AGCC TGCGCTCCGT ACCTGCGTA TG----- | | |
| 87 ORF 03 | A | CATGGAACTA GATATT AACC GGTTCCGCGG ATCCCATGCA TG----- | | 27 |
| 88 | B | CATGGAACTA GATAAT AACC GGTCGGCGG GTACAATGCA TG----- | | |
| 89 PPI | A | ATACCGAGAA GTTATA GCAG GGTATGGAAT GTGCGCCGC ATG----- | | 28 |
| 90 | B | AGCACGACAA GTTATA GCAG GGTACAAAGG AGCAGCGCAC ATG----- | | |
| 91 GSAT | A | ATCCGCCCTG ATTTAA TTAT GGGGGGAGCG GCCTGCTGCC GTG----- | | 28 |
| 92 | B | ATCCGGCCCTC ATTTAA TTAC GGGGGGTACA ACCTGCTGCC GTG----- | | |
| 93 ORF 05 | A | CCTTCATACA CATAAA TCCC GCTTGGATGT GCGGCTGCGC ATG----- | | 28 |
| 94 | B | ACTTCATACA CATAAA TCCC GCCTGAACGG TCGTCCGCG ATG----- | | |
| 95 deaminase | A | GGCATATAC CATAAT ATGC CGGGCGGTGG CACCATGGCC GTT----- | | 29 |
| 96 | B | CCGCATATAC CATAAT ATGC CGGGCGGGGG CAGGCTGCC .GTG----- | | |
| 97 RNA helic | A | TGTACGAAC CATAAA ACAA CAGGCGCGT CAGGGCCGCG CGT----- | | 29 |
| 98 | B | GGGTAGAAC CATAAA ACAA CAGGCGCGG CAGGGCG.CG CGT----- | | |
| 99 ORF 06 | A | ACACGCAG TATAAA CGGG GCCCCGGCG GCGCGTATCA CATG----- | | 29 |
| 100 | B | ATACACGTGG TATAAA CAGA GG.CCGACG GCGCGGACCA CATG----- | | |
| 101 tRNA-tyr | A | GCGATAGTTA TTTAAA ACTA GGATGCCAT CACGGATCGT CCCA----- | | 29 |
| 102 | B | GCGATAGTTA TTTAAA ACTA GGATGCCGGG CACCGTCGT CCCA----- | | |
| 103 TBP | A | CCGGGCCCG GTTAAA ATAG CG.CACGGGC GGATCCTGAC CAATG----- | | 30 |
| 104 | B | CCGGGCCCG GTTAAA ATAG AGTGGGGCGG GGCACCGGAT CAATG----- | | |
| 105 TIM | A | GCGTCGATAG AATAAA TACG CGCAGGGGC CCCGTGGCG GATGCCCGT G----- | | 36 |
| 106 | B | GCGTCGATAG AATAAA TACG CGC.GGGGC GCGGTGC... GATGCCCGT G----- | | |
| 107 Hypoth 01 | A | ATTTCAACTA CATAAA TGCC TAGTACGCA GAAATAGCAA ACGACGTACT TCGACTAATG | 45 | |
| 108 | B | ACTTCAACTA CATAAA TGCC TAGTACGCA GAAATATCAA ACAAAGTACT TCGACTAATG | | |
| 109 ORF 01 | A | ACGGCAGGCT ATTATT ACCT TGCCCTGCCT TGTA //.. G CGGGTGCAG CAGGGGATG | 52 | |
| 110 | B | ACGGCAGGCT ATTATT ACCT TGCGTGTG. TACA //.. G ACGGGGCGCTG CGGGGAGTG | | |
| 111 Methylase | A | CTACAACGAT TTTAAG TCGG CGCCGGGGCA GCCG.//.. G ATGTGGGCA GGCAACATG | 104 | |
| 112 | B | CTACAACGAT TTTAAG ACGG CGCGGTGCC CGCG.//.. T GGCACGGGG CCTATCTG | | |
| 113 16S RNA | A | TCGGCGATGG TTTATA TGCC CATGGACGGG CGATCCGAT CGTACGTGAC GC.//.. AAT | 220 | |
| 114 | B | CCGGCGATGG TTTATA TGCC CATGGACAAG GCGATCCGAT CGTACGTGAC GC.//.. AAT | | |
| Archaeal promoter consensus | | | | |
| | | YTTAWA | | |

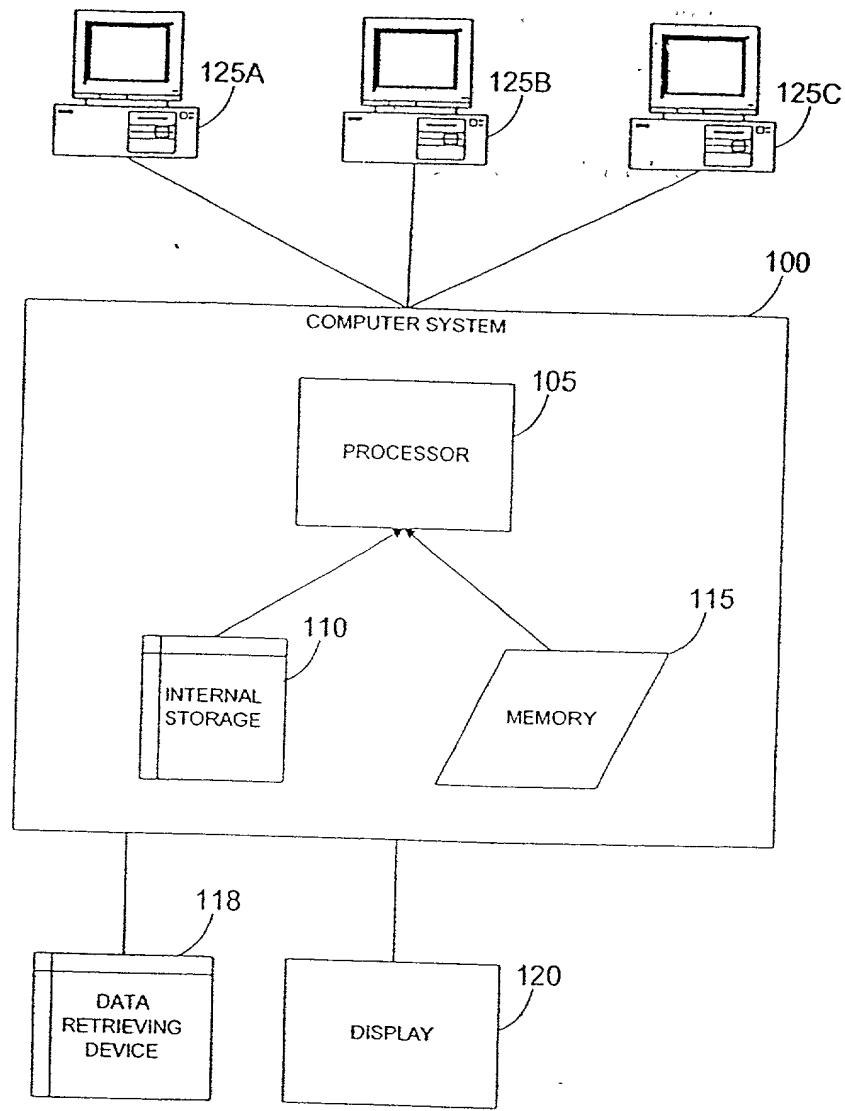


FIGURE 3

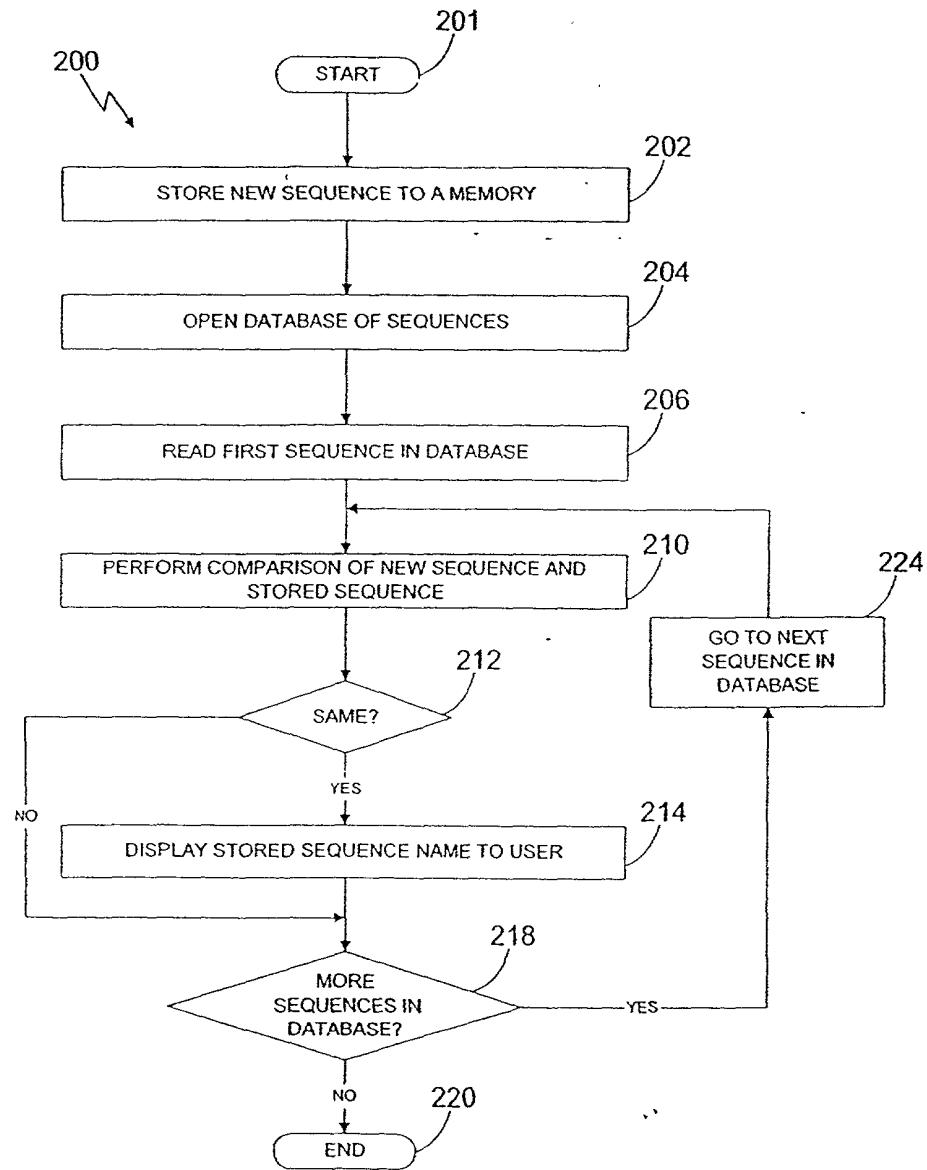


FIGURE 4

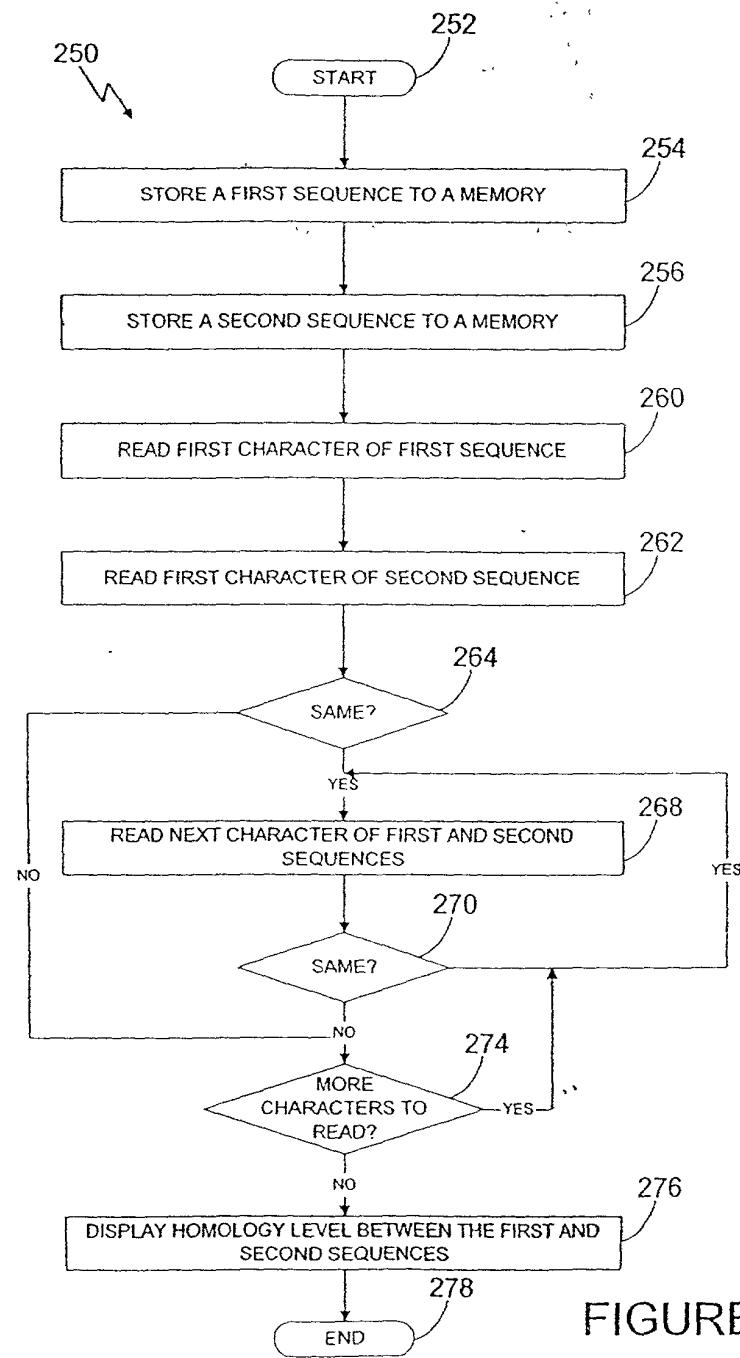


FIGURE 5

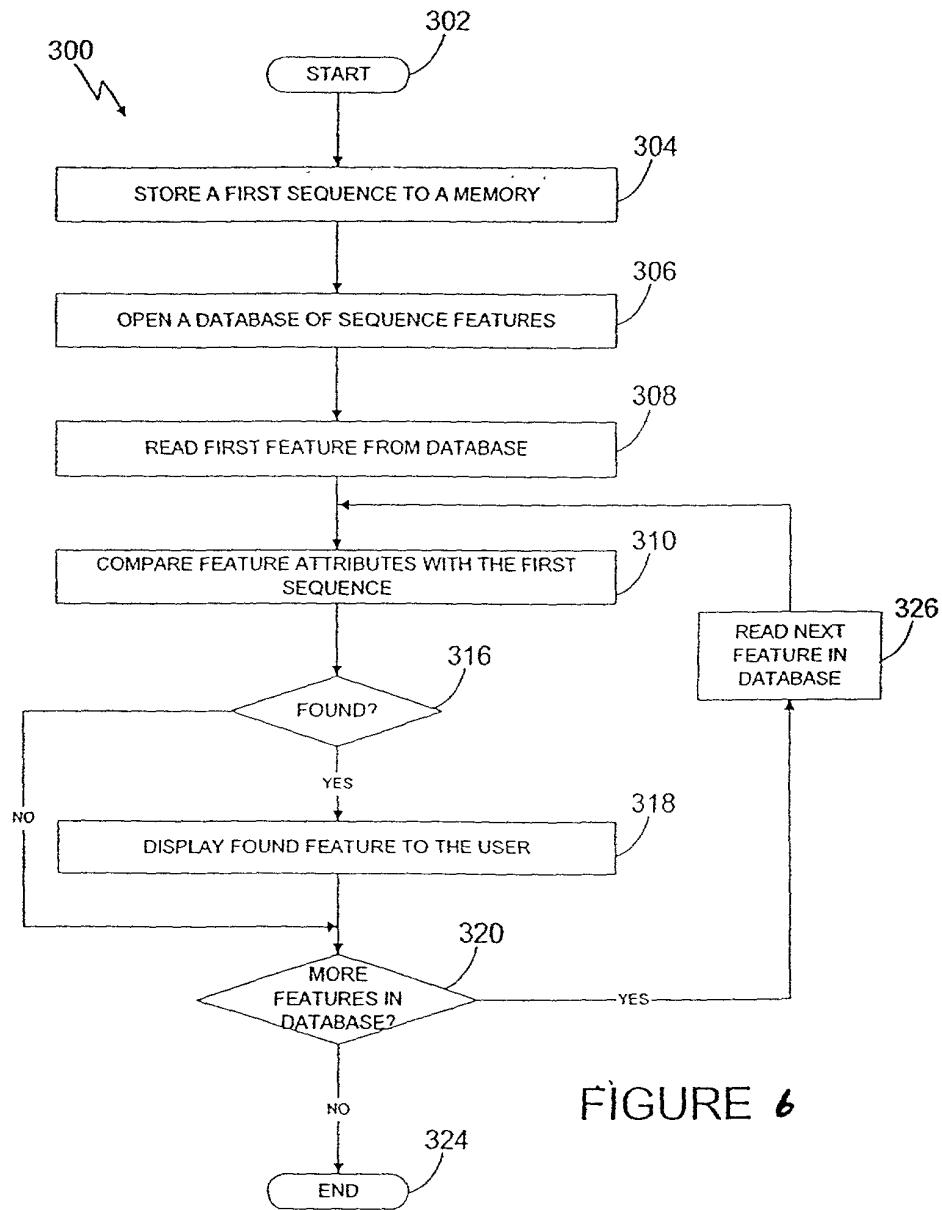


FIGURE 6